

Filename : Phrixothrix vivianii lateral lanterns green light-eliciting  
luciferase cDNA and deduced primary structure.  
Sequence Size : 1746  
Sequence Position: -25 - 1746

Translation Position: 1 - 1635;

Genetic Code : Universal (amino-acid residues are in 3 letter code)

-20                      -10  
TCAGTGAAGACTTTAGGG

10                      20                      30                      40                      50  
ATCAAAATGGAGAGAAACATTAGGCATGGAGAGCGTCCTCGTGATATAGTCCATCCT  
MetGluGluGluAsnIleArgHisGlyGluArgProArgAspIleValHisPro

60                      70                      80                      90                      100                      110  
GGCTCGGCAGGACAACAATTATACCAATCATTGTATAAATTTGCATCTTTTCCTGAAGCA  
GlySerAlaGlyGlnGlnLeuTyrGlnSerLeuTyrLysPheAlaSerPheProGluAla

120                      130                      140                      150                      160                      170  
ATAATCGATGCTCATACAATGAAGTAATATCATATGCTCAATATTTGAAACCAGCTGC  
IleIleAspAlaHisThrAsnGluValIleSerTyrAlaGlnIlePheGluThrSerCys

180                      190                      200                      210                      220                      230  
CGCTTAGCTGTTAGTATAGAACAATATGGCTTGAATGAAARCAATGTTGTGGGTGTATGC  
ArgLeuAlaValSerIleGluGlnTyrGlyLeuAsnGluAsnAsnValValGlyValCys

240                      250                      260                      270                      280                      290  
AGTGAAACCAATATAAACTTTTTTAAATCCTGTCCTTGCTGCTTTATACCTTAGGAATACCA  
SerGluAsnAsnIleAsnPhePheAsnProValLeuAlaAlaLeuTyrLeuGlyIlePro

300                      310                      320                      330                      340                      350  
GTAGCAACATCAAAATGATATGTACACAGATGGAGAGTTAAGTGGTCATTTGAATATATCA  
ValAlaThrSerAsnAspMetTyrThrAspGlyGluLeuThrGlyHisLeuAsnIleSer

360                      370                      380                      390                      400                      410  
AAACCAACTATCATGTTTGTAGTTCAAAGAAAGCACTCCCGCTTATTCTGAGAGTACAGCAA  
LysProThrIleMetPheSerSerLysLysAlaLeuProLeuIleLeuArgValGlnGln

420                      430                      440                      450                      460                      470  
AATCTAAGTTTCAATTAAGTTCGTAGTTATCGATAGCATGTACGACATTAATGGCGTT  
AsnLeuSerPheIleLysLysValValValIleAspSerMetTyrAspIleAsnGlyVal

480                      490                      500                      510                      520                      530  
GAATGCGTATCTACCTTTGTTGCACGTTAFACTGACCACACCTTTGATCCATTGTCAATTT  
GluCysValSerThrPheValAlaArgTyrThrAspHisThrPheAspProLeuSerPhe

540                      550                      560                      570                      580                      590  
ACACCAAAAGATTTTGATCCCTTGAAAAATCGCATTAAATTATGTATCATCTGGAACA  
ThrProLysAspPheAspProLeuGluLysIleAlaLeuIleMetSerSerSerGlyThr

FIG. 1A

600 610 620 630 640 650  
ACTGGATTGCCTAAGGGTGTAGTACTGAGCCATAGAAGTCTAACTATAAGATTTCGTTTCAT  
ThrGlyLeuProLysGlyValValLeuSerHisArgSerLeuThrIleArgPheValHis

660 670 680 690 700 710  
AGCAGGGATCCCATTTATGGCACTCGTACGGTTCACAAACATCAATTCTTTCCTTAGTA  
SerArgAspProIleTyrGlyThrArgThrValProGlnThrSerIleLeuSerLeuVal

720 730 740 750 760 770  
CCGTTCCATCATGCCTTTGGAATGTTTACTACATTATCTTACTTTGTAGTAGGACTTAAG  
ProPheHisHisAlaPheGlyMetPheThrThrLeuSerTyrPheValValGlyLeuLys

780 790 800 810 820 830  
GTTGTAATGTTGAAGAAATTTGAGGGCGCACTTTTCTTAAAAACCATACAGAATTACAAA  
ValValMetLeuLysLysPheGluGlyAlaLeuPheLeuLysThrIleGlnAsnTyrLys

840 850 860 870 880 890  
ATCCCCACTATTGTAGTGGCCCCCTCCAGTTATGGTGTTTTTGGCTAAAGCCCCATTAGTC  
IleProThrIleValValAlaProProValMetValPheLeuAlaLysSerProLeuVal

900 910 920 930 940 950  
GATCAATACGATTTATCGAGCTTAACGGAAGTTGCTACTGGAGGAGCTCCTTTAGGAAAA  
AspGlnTyrAspLeuSerSerLeuThrGluValAlaThrGlyGlyAlaProLeuGlyLys

960 970 980 990 1000 1010  
GATGTCCGAGAAGCAGTAGCAGAAGAGGTTGAAATTACCTGGATCATAACAAGGATATGGA  
AspValAlaGluAlaValAlaLysArgLeuLysLeuProGlyIleIleGlnGlyTyrGly

1020 1030 1040 1050 1060 1070  
TTAACTGAAACTTGCTGCGCTGTAATGATTACCCCTCATATGCTGTGAAACAGGTTCA  
LeuThrGluThrCysCysAlaValMetIleThrProHisAsnAlaValLysThrGlySer

1080 1090 1100 1110 1120 1130  
ACTGGAAGACCCTTGCCATACATTAAAGCTAAAGTTTTAGATAACGCTACTGGGAAGGCG  
ThrGlyArgProLeuProTyrIleLysAlaLysValLeuAspAsnAlaThrGlyLysAla

1140 1150 1160 1170 1180 1190  
CTAGGACCAGGAGAAAGAGGCGAAATATGCTTTCAAAGTGAAATGATTATGAAAGGATAT  
LeuGlyProGlyGluArgGlyGluIleCysPheGlnSerGluMetIleMetLysGlyTyr

1200 1210 1220 1230 1240 1250  
TACAACAATCCGGAAGCAACTATTGATACTATTGACAAAGATGCTTGGCTTCATTCTGGA  
TyrAsnAsnProGluAlaThrIleAspThrIleAspLysAspGlyTrpLeuHisSerGly

1260 1270 1280 1290 1300 1310  
GATATTGGATATTACGACGAAGATGGAATTTCTTTATAGTTGATCGATTGAAAGAACTT  
AspIleGlyTyrTyrAspGluAspGlyAsnPhePheIleValAspArgLeuLysGluLeu

1320 1330 1340 1350 1360 1370  
ATTAAATACAAGGGATATCAGGTTGCGCCTGCTGAACTGGAAATCTGCTTTTACAACAT  
IleLysTyrLysGlyTyrGlnValAlaProAlaGluLeuGluAsnLeuLeuLeuGlnHis

1380 1390 1400 1410 1420 1430  
CCAAGTATTGCTGATGCGGGTGTTACTGGAGTTCCGGACGAATTTGGTGGACAATTACCT  
ProSerIleAlaAspAlaGlyValThrGlyValProAspGluPheGlyGlyGlnLeuPro

FIG. 1B

1440 1450 1460 1470 1480 1490  
GCTGCTTGTGTTGTGTTAGAATCTGGCAAGACGCTGACTGAAAAGGAAGTTCAAGATTTT  
AlaAlaCysValValLeuGluSerGlyLysThrLeuThrGluLysGluValGlnAspPhe

1500 1510 1520 1530 1540 1550  
ATTGCAGCACAAAGTCACTCCAACAAAGCATCTTCGAGGCGGTGTCGTATTTGTAGACAGT  
IleAlaAlaGlnValThrProThrLysHisLeuArgGlyGlyValValPheValAspSer

1560 1570 1580 1590 1600 1610  
ATTCCGAAAGGCCCTACTGGAAACTCATCAGAAAGGAGCTCCGAGAAATATTTGCCCAG  
IleProLysGlyProThrGlyLysLeuIleArgLysGluLeuArgGluIlePheAlaGln

1620 1630 1640  
CGAGCACCAAAATCAAAATTATAAGTTCAATGTATTGCTTTAGTTCTAAAATGTATATAA  
ArgAlaProLysSerLysLeu\*\*\*

ACAAGTTTTAGAACCTAATACATTCAATCAATACTAAACAAAAAAAAAAAAAAAAAAAAA  
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Filename : PhRECDNA  
Sequence Size : 1720  
Sequence Position: -40 - 1760  
Translation Position: 1 - 1638;  
Genetic Code : Universal (amino-acid residues in 1 letter code)

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                -30      -20      -10
      GTGACAGTTTAGTTTCAGTAGAAGATTTTTTTTGGATCAAA

      10      20      30      40      50      60
ATGGAAGAAGAAAACGTTGTGAATGGAGATCGTCCTCGTGATCTAGTTTTTCCTGGCACA
M E E E N V V N G D R P R D L V F P G T

      70      80      90      100     110     120
GCAGGACTACAATTATATCAATCATTATATAAATATTCATATATTACTGACGGAATAATC
A G L Q L Y Q S L Y K Y S Y I T D G I I

      130     140     150     160     170     180
GATGCCCATACCAATGAAGTAATATCATATGCTCAAATATTTGAAACCAGCTGCCGCTTG
D A H T N E V I S Y A Q I F E T S C R L

      190     200     210     220     230     240
GCAGTTAGTCTAGAAAAATATGGCTTGGATCAATAACAAATGTTGTGGCAATATGCAGTGAA
A V S L E K Y G L D H N N V V A I C S E

      250     260     270     280     290     300
AACAAACATACACTTTTTTGGCCCTTTAATTGCTGCTTTATACCAAGGAATACCAATGGCA
N N I H F F G P L I A A L Y Q G I P M A

      310     320     330     340     350     360
ACATCAATGATATGTACACAGAAAGGGAGATGATTGCCCATTTGAATATATCGAAACCA
T S N D M Y T E R E M I G H L N I S K P

      370     380     390     400     410     420
TGCCTTATGTTTTGTTCAAGAAATCACTCCCATTTATTCTGAAAGTACAAAAACATCTA
C L M F C S K K S L P F I L K V Q K H L

      430     440     450     460     470     480
GATTCCTTAAAGAGTCATAGTCATTGATAGTATGTACGATATCAATGGCGTTGAATGC
D F L K R V I V I D S M Y D I N G V E C

      490     500     510     520     530     540
GTATTTAGCTTTGATTCACGTAATACTGATCAGCGCTTTGATCCAGTGAAATTTAACCCA
V F S F D S R N T D H A F D P V K F N P

      550     560     570     580     590     600
AAAGAGTTTGATCCCTTGGAAGAAGACCGCATTAATTATGACATCATCTGGAACAACCTGGA
K E F D P L E R T A L I M T S S G T T G

      610     620     630     640     650     660
TTGCCTAAAGGGGTAGTAATAAGCCATAGAAGTATAACTATAAGATTTCGTCCATAGCAGT
L P K G V V I S H R S I T I R F V H S S
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FIG. 2A

670 680 690 700 710 720  
GATCCCATCTATGGTACTCGTATTGCTCCAGATACATCAATTCTTGCTATAGCACCGTTC  
D P I Y G T R I A P D T S I L A I A P F

730 740 750 760 770 780  
CATCATGCCCTTTGGACTGTTTACTGCAC TAGCTTACTTTCCAGTAGGACTTAAGATTGTA  
H H A F G L F T A L A Y F P V G L K I V

790 800 810 820 830 840  
ATGGTGAGAAATTTGAGGGCGAATTCTTCTTAAACCATACAAAATTACAAAATCGCT  
M V K K F E G E F F L K T I Q N Y K I A

850 860 870 880 890 900  
TCTATTGTAGTTCCTCCTCCAATTATGGTATATTTGGCTAAAAGTCCATTAGTCGATGAA  
S I V V P P P I M V Y L A K S P L V D E

910 920 930 940 950 960  
TACAATTGCTCGAGCTTAACGGAAATTGCTAGTGGAGGCTCTCCTTTAGGAAGAGATATC  
Y N C S S L T E I A S G G S P L G R D I

970 980 990 1000 1010 1020  
GCAGATAAAGTAGCAAAGAGATTGAAAGTACATGGAATCCTACAAGGATATGGATTAAACC  
A D K V A K R L K V H G I L Q G Y G L T

1030 1040 1050 1060 1070 1080  
GAAACCTGCAGCGCTCTAATACTTAGCCCCAATGATCGAGAATTAATAAAGGTGCAATT  
E T C S A L I L S P N D R E L K K G A I

1090 1100 1110 1120 1130 1140  
GGAACGCCTATGCCATATGTTCAAGTTAAAGTTATAGATATCAATACTGGGAAGGCGCTA  
G T P M P Y V Q V K V I D I N T G K A L

1150 1160 1170 1180 1190 1200  
GGACCAAGAGAAAAAGGCGAATATGCTTCAAAAGTCAATGCTTATGAAAGGATATCAC  
G P R E K G E I C F K S Q M L M K G Y H

1210 1220 1230 1240 1250 1260  
AACAAATCCGCAAGCAACTCGTGATGCTCTTGACAAAGATGGTTGGCTTCATACTGGGGAT  
N N P Q A T R D A L D K D G W L H T G D

1270 1280 1290 1300 1310 1320  
CTTGGATATTACGACGAAGACAGATTTATCTATGTAGTTGATCGATTGAAAGAACTTATT  
L G Y Y D E D R F I Y V V D R L K E L I

1330 1340 1350 1360 1370 1380  
AAATATAAAGGATATCAGGTTGCGCCTGCTGAACCTGGAAATCTGCTTTTACAACATCCA  
K Y K G Y Q V A P A E L E N L L L Q H P

1390 1400 1410 1420 1430 1440  
AATATTTCTGATGCGGGTGTTATTGAATTCGGGACGAATTTGCTGGTCAATTACCTTTCC  
N I S D A G V I E F R T N L L V N Y L S

1450 1460 1470 1480 1490 1500  
GCGTGTGTTGTGTAGAGCCTGGTAAGACATGACCGAAAAGGAAGTTCAGGATTATATT  
A C V V L E P G K T M T E K E V Q D Y I

FIG. 2B

1510 1520 1530 1540 1550 1560  
GCAGAGCTAGTCACTACAACATAACATCTTCGAGGCGGTGTCGTATTTATAGATAGTATT  
A E L V T T T K H L R G G V V F I D S I

1570 1580 1590 1600 1610 1620  
CCAAAAGGCCCAACAGGAAACTCATGAGAAACGAACTCCGAGCAATATTTGCCCCGGGAA  
P K G P T G K L M R N E L R A I F A R E

1630 1640 1650 1660 1670 1680  
CAGGCAAAATCAAATTATAAGCTCAATATATTGCTTTAGTTATAAAATGTATGTAATCA  
Q A K S K L \*

1690 1700 1710 1720  
AATTTTAGAACCTAATACATTGAGAGCCTAAAAAA

FIG. 2C

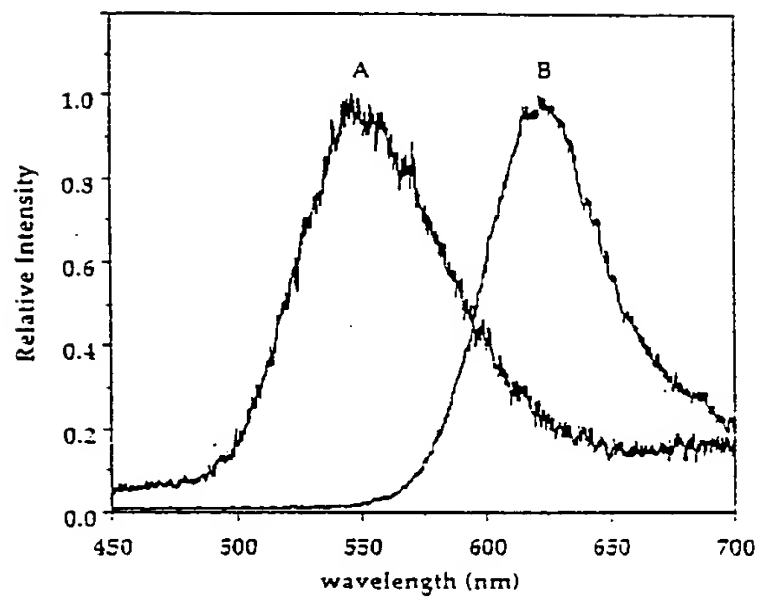


FIG. 3